

NATURE 2001

83% identity to SEQ ID NO:1 but not annotated as sphingomyelinase

<!--StartFragment--> NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Placenta, and Intestinal mucosa;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
 RA Hayashizaki Y.;  
 =====> RT "Functional annotation of a full-length mouse cDNA collection.";  
 =====> RL Nature 409:685-690(2001).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta, and Intestinal mucosa;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [7]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta, and Intestinal mucosa;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwake S., Inoue K., Togawa Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system--384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Placenta;  
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.  
 RN [9]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Intestinal mucosa;  
 RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
 RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,

RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,  
 RA Muramatsu M., Hayashizaki Y.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.  
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 CC -----  
 DR EMBL; AK144474; BAE25908.1; -; mRNA.  
 DR EMBL; AK167678; BAE39727.1; -; mRNA.  
 DR UniGene; Mm.244114; -.  
 DR Ensembl; ENSMUSG00000046697; Mus musculus.  
 DR MGI; MGI:3027917; Enpp7.  
 DR GO; GO:0008152; P:metabolic process; IEA:InterPro.  
 DR InterPro; IPR001952; Alk\_phosphtse. it is not annotated as sphingomyelinase  
 DR InterPro; IPR002591; Phosphodiester.  
 DR Gene3D; G3DSA:3.40.720.10; Alk\_phosphtse; 1.  
 DR Pfam; PF01663; Phosphodiester; 1.  
 PE 2: Evidence at transcript level;  
 SQ SEQUENCE 439 AA; 49618 MW; 5D6112A945136709 CRC64;

Query Match 75.6%; Score 1868.5; DB 2; Length 439;  
 Best Local Similarity 82.9%; Pred. No. 2e-137;  
 Matches 343; Conservative 34; Mismatches 34; Indels 3; Gaps 1;

Qy	5 AVLLTVALATLLAPGAGAPVQSQGSQNKL禄VSDGFRWNYDQDVDTPLNDAMARDGVKA 64
	:                 :   :
Db	5 AVLLCVALAILPACVTGAPVQ--RQHKLLLVSFDGFRWNYDQDVDTPLNLDMAQEGVKA 61

Qy	65 RYMTPAFVTMTSPCHFTLVTGKYIENHGVVHNMYYNTTSKVKLPYHATLGIQRWWDNGSV 124
	:                  :      :      :      :      :
Db	62 QYMTPAFVTMTSPCHFTLVTGKYIENHGVVHNMFYNTTSTVRLPYHATLGIQRWWDNGSI 121

Qy	125 PIWITAQRQGLRAGSFFYPGGNVTYQGVAVTRSKEGIAHNYKNETEWRANIDTVMAWFT 184
	:                         :            :
Db	122 PIWITAQRQGLKTGSFFYPGGNVTYQGEAVTMSRKEGVLHNYKNETEWRGNVDTVMKWFL 181

Qy	185 EEDLDLVTLYFGEPDSTGHRYGPESPERREMVRQVDRTVGYLRESIARNHLDRLNLIIIT 244
	:               :         :   :         :   :
Db	182 EEDVSLVTLYFGEPDSTGHKYGPESQERKDMVKQVDRTVGYLRSIKRHHLSDSLNLIIT 241

Qy	245 SDHGMTTVDKRAGDLVEFHKFPLTFRDIEFELLDYGPNGMLLPKEGRLEKVDALKDAH 304
	: :            :   :         :   :
Db	242 SDHGMTTVNKKASDLVEFHKSNTFQDIQFELLDYGPIGMLIPKEGMLEKVYSVLDAH 301

Qy	305 PKLHVYKKEAFPEAFHYANNPRVTPLLMSDLGYVIHGRINVQFNNGEHGFDNKDMDMKT 364
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Db	302 PRLHVYKKEDFPKNFHYANNPRITPLLMSDLGYVIHGRNVQFNNGEHGFNNQDMDMKT 361

Qy	365 IFRAVGPSFRAGLEVFPFESVHVFYELMCRLLGIVPEANDGHLATLLPMLHTESA 418
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Db	362 IFRAVGPSFKAGLEVFPFESVHVFYELMCQLLGIVPEPNNDGNPGILRPMLRSGSA 415

RESULT 5

&lt;!--EndFragment--&gt;